

GenCore version 5.1.6  
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(without alignments)  
7315.604 Million cell updates/sec

Title: US-10-054-399A-1  
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Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3          | 228   | 100.0 | 228    | 6  | E61227    | E61227 Nucleotide   |
| 4          | 226.4 | 99.3  | 228    | 6  | AX004385  | AX004385 Sequence   |
| 5          | 226.4 | 99.3  | 228    | 6  | AX004387  | AX004387 Sequence   |
| 6          | 226.4 | 99.3  | 228    | 6  | AX004389  | AX004389 Sequence   |
| 7          | 226.4 | 99.3  | 228    | 6  | BD078524  | BD078524 Yeast Cdc  |
| 8          | 226.4 | 99.3  | 228    | 6  | BD078525  | BD078525 Yeast Cdc  |
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| 17         | 105.6 | 46.3  | 3908   | 8  | AF210636  | AF210636 Fremothec  |
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| 22         | 42.8  | 18.8  | 37301  | 8  | SPAC16E8  | 298529 S.pombe chr  |
| 23         | 41    | 18.0  | 138668 | 8  | AC092749  | AC092749 Genomic s  |
| 24         | 41    | 18.0  | 300029 | 8  | AE017081  | AE017081 Oryza sat  |
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| C 27       | 38    | 16.7  | 489    | 11 | G06443    | G06443 human STS W  |
| C 28       | 38    | 16.7  | 1243   | 9  | HSR803058 | AL713781 Homo sapi  |
| C 29       | 38    | 16.7  | 1506   | 6  | A27284    | A27284 H.sapiens T  |
| C 30       | 38    | 16.7  | 1596   | 9  | BC008895  | BC008895 Homo sapi  |
| C 31       | 38    | 16.7  | 1808   | 9  | AK093731  | AK093731 Homo sapi  |
| C 32       | 38    | 16.7  | 2109   | 9  | HSTGR1    | X72018 H.sapiens h  |
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| C 34       | 38    | 16.7  | 2457   | 9  | HUM4PRO   | L03532 Human M4 pr  |
| C 35       | 38    | 16.7  | 2514   | 9  | BC000138  | BC000138 Homo sapi  |
| C 36       | 38    | 16.7  | 2542   | 9  | BC019580  | BC019580 Homo sapi  |
| C 37       | 38    | 16.7  | 18889  | 9  | AL513476  | AL513476 Human DNA  |
| C 38       | 38    | 16.7  | 74932  | 9  | AC008762  | AC008762 Homo sapi  |
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| C 42       | 37.6  | 16.5  | 2453   | 9  | AF061832  | AF061832 Homo sapi  |
| C 43       | 37.4  | 16.4  | 79174  | 9  | AL356372  | AL356372 Human DNA  |
| C 44       | 37.4  | 16.4  | 167574 | 2  | AC011274  | AC011274 Homo sapi  |
| C 45       | 37.2  | 16.3  | 177048 | 2  | AC128925  | AC128925 Rattus no  |

ALIGNMENTS

|            |            |                                   |                                   |        |     |        |                 |
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| RESULT 1   | AX004383   | AX004383                          | Sequence 1 from Patent WO9918213. | 228 bp | DNA | linear | PAT 24-AUG-2000 |
| LOCUS      | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
| DEFINITION | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
| ACCESSION  | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
| VERSION    | AX004383.1 | GI:9927860                        |                                   |        |     |        |                 |
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| ORGANISM   | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
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| AUTHORS    | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
| TITLE      | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |
| JOURNAL    | AX004383   | Sequence 1 from Patent WO9918213. |                                   |        |     |        |                 |

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LOCUS      BD078523      228 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.
ACCESSION  BD078523
VERSION     BD078523.1 GI:22624126
KEYWORDS   JP 2001519158-A/1
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1 (bases 1 to 228)
AUTHORS   Arkowitz,R.A. and Nern,P.M.A.
TILE       Patent: JP 2001519158-A 1 23-OCT-2001;
JOURNAL    MEDICAL RESEARCH COUNCIL
COMMENT    OS Artificial Sequence
            PN JP 2001519158-A/1
            PD 23-OCT-2001
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            PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR
            PI ROBERT ALAN ARKOWITZ,PETER MICHAEL ALJOSCHA NERN PC
            CI2N15/09,A61K38/00,A61K45/00,A61P43/00,C07K14/82,C12Q1/68, PC
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DEFINITION Nucleotide sequence and protein sequence.
ACCESSION  E61227
VERSION     E61227.1 GI:13027197
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SOURCE     unidentified
            unclassified.
REFERENCE  1 (bases 1 to 228)
AUTHORS   Robert,A.A. and Pater,M.A.N.
TILE       Nucleotide sequence and protein sequence
JOURNAL    Patent: JP 1999113578-A 1 27-APR-1999;
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COMMENT    OS Unidentified
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            PD 27-APR-1999
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ACCESSION  E61227
VERSION     E61227.1 GI:13027197
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SOURCE     unidentified
            unclassified.
REFERENCE  1 (bases 1 to 228)
AUTHORS   Robert,A.A. and Pater,M.A.N.
TILE       Nucleotide sequence and protein sequence
JOURNAL    Patent: JP 1999113578-A 1 27-APR-1999;
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ACCESSION AX004385
VERSION AX004385.1 GI:9927861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 3 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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VERSION AX004387.1 GI:9927862
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artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 5 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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DEFINITION Sequence 7 from Patent WO9918213.
ACCESSION AX004389
VERSION AX004389.1 GI:9927863
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Nern,P.M. and Arkowitz,R.A.
AUTHORS Mutants of yeast cdc24p, defective in binding of the g-protein beta
TITLE subunit
JOURNAL Patent: WO 9918213-A 7 15-APR-1999;
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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BD078524
LOCUS BD078524 228 bp DNA linear PAT 27-AUG-2002
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.
ACCESSION BD078524
VERSION BD078524.1 GI:22624127
KEYWORDS
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ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
AUTHORS Arkowitz,R.A. and Nern,P.M.A.  
TITLE Yeast Cdc24p variant lacking G protein beta-subunit bond  
JOURNAL Patent: JP 2001519158-A 2 23-OCT-2001;  
MEDICAL RESEARCH COUNCIL  
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12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09, A61K45/00, A61P43/00, C07K14/82, C12Q1/68, PC  
G01N33/566,  
PC C12N15/00, A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228 /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228 /organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
BASE COUNT 68 a 48 c 42 g 70 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
DB 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
QY 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
DB 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
QY 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAACTCGAGCTCC 180  
DB 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAACTCGAGCTCC 180  
QY 181 CAGCTGTGCAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
DB 181 CAGCTGTGCAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
RESULT 8  
BD078525  
LOCUS BD078525 228 bp DNA linear PAT 27-AUG-2002  
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078525  
VERSION BD078525.1 GI:22624128  
KEYWORDS JP 2001519158-A/3.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 3 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/3  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3, 08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09, A61K45/00, A61P43/00, C07K14/82, C12Q1/68, PC

G01N33/566,  
PC C12N15/00, A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228 /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228 /organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
BASE COUNT 67 a 49 c 43 g 69 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
DB 1 CCCCTCTGTATACITTTCAACTCTGTGAAGCGCGCAATTTAAATACCGGTAATAGCATCT 60  
QY 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
DB 61 GACGATTGAAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAAACAC 120  
QY 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAACTCGAGCTCC 180  
DB 121 TTTCGATTACGATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCAACTCGAGCTCC 180  
QY 181 CAGCTGTGCAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
DB 181 CAGCTGTGCAAGTCTGTAGAGTAGTAGAAGCGCTAATGAATCCAGC 228  
RESULT 9  
BD078526  
LOCUS BD078526 228 bp DNA linear PAT 27-AUG-2002  
DEFINITION Yeast Cdc24p variant lacking G protein beta-subunit bond.  
ACCESSION BD078526  
VERSION BD078526.1 GI:22624129  
KEYWORDS JP 2001519158-A/4.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 228)  
REFERENCE Arkowitz,R.A. and Nern,P.M.A.  
AUTHORS Yeast Cdc24p variant lacking G protein beta-subunit bond  
TITLE Patent: JP 2001519158-A 4 23-OCT-2001;  
JOURNAL MEDICAL RESEARCH COUNCIL  
COMMENT OS Artificial Sequence  
PN JP 2001519158-A/4  
PD 23-OCT-2001  
PF 08-OCT-1998 JP 2000515009  
PR 08-OCT-1997 GB 9721357.3, 08-OCT-1997 GB 9721358.1 PR  
12-JUN-1998 GB 9812793.9  
PI ROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC  
C12N15/09, A61K45/00, A61P43/00, C07K14/82, C12Q1/68, PC  
G01N33/566,  
PC C12N15/00, A61K37/02  
CC Description of Artificial Sequence: nucleic acid FH Key  
FT Location/Qualifiers  
FT source 1..228 /organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..228 /organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
BASE COUNT 68 a 50 c 42 g 68 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;

Best Local Similarity 99.6%; Pred. No. 2.3e-52;

Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
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Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCACCT 60  
|||||  
QY 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||  
Db 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||  
QY 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||  
Db 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||  
QY 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||  
Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

RESULT 10  
E61228 LOCUS 228 bp DNA linear PAT 18-JUN-2001  
DEFINITION Nucleotide sequence and protein sequence.  
E61228  
ACCESSION  
VERSION F61228.1 GI:13027198  
KEYWORDS JP 1999113578-A/2.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE  
AUTHORS Robert,A.A. and Pater,M.A.N.  
TITLE Nucleotide sequence and protein sequence  
JOURNAL Patent: JP 1999113578-A 2 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT  
PN JP 1999113578-A/2  
PD 27-APR-1999 JP 1997326899  
PF 21-OCT-1997 GB 9721358:1  
PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC  
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/B2,G01N33/15, PC  
C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FEATURES  
source

BASE COUNT 68 a 48 c 42 g 70 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
|||||  
Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATTT 60  
|||||

QY 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||  
Db 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||

QY 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||  
Db 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||

QY 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||

RESULT 12  
E61230 LOCUS 228 bp DNA linear PAT 18-JUN-2001  
DEFINITION Nucleotide sequence and protein sequence.  
E61230  
ACCESSION  
VERSION E61230.1 GI:13027200  
KEYWORDS JP 1999113578-A/4.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE  
AUTHORS Robert,A.A. and Pater,M.A.N.  
TITLE Nucleotide sequence and protein sequence  
JOURNAL Patent: JP 1999113578-A 3 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT  
PN JP 1999113578-A/3  
PD 27-APR-1999 JP 1997326899  
PF 21-OCT-1997 GB 9721358:1  
PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC  
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/B2,G01N33/15, PC  
C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FEATURES  
source

BASE COUNT 68 a 48 c 42 g 70 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
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Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATTT 60  
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Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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RESULT 11  
E61229 LOCUS 228 bp DNA linear PAT 18-JUN-2001  
DEFINITION Nucleotide sequence and protein sequence.  
E61229  
ACCESSION  
VERSION E61229.1 GI:13027199  
KEYWORDS JP 1999113578-A/3.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE  
AUTHORS Robert,A.A. and Pater,M.A.N.  
TITLE Nucleotide sequence and protein sequence  
JOURNAL Patent: JP 1999113578-A 3 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT  
PN JP 1999113578-A/3  
PD 27-APR-1999 JP 1997326899  
PF 21-OCT-1997 GB 9721358:1  
PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC  
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/B2,G01N33/15, PC  
C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FEATURES  
source

BASE COUNT 67 a 49 c 43 g 69 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
|||||  
Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
|||||

QY 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||  
Db 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
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QY 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||  
Db 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||

QY 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||  
Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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RESULT 12  
E61230 LOCUS 228 bp DNA linear PAT 18-JUN-2001  
DEFINITION Nucleotide sequence and protein sequence.  
E61230  
ACCESSION  
VERSION E61230.1 GI:13027200  
KEYWORDS JP 1999113578-A/4.  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE  
AUTHORS Robert,A.A. and Pater,M.A.N.  
TITLE Nucleotide sequence and protein sequence  
JOURNAL Patent: JP 1999113578-A 3 27-APR-1999;  
MEDICAL RESEARCH COUNCIL

COMMENT  
PN JP 1999113578-A/3  
PD 27-APR-1999 JP 1997326899  
PF 21-OCT-1997 GB 9721358:1  
PI ROBERT ALAN AKOVITTSU,PATER MICHAEL ARUYOSHA NERUN PC  
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/B2,G01N33/15, PC  
C12N15/00,  
PC A61K37/02

CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..228 /organism='Unidentified'.  
FEATURES  
source

BASE COUNT 67 a 49 c 43 g 69 t  
ORIGIN  
Query Match 99.3%; Score 226.4; DB 6; Length 228;  
Best Local Similarity 99.6%; Pred. No. 2.3e-52;  
Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
|||||  
Db 1 CCCCTCTGTATCTTTTCAACTCTGTGAAGCGGCAATTAAATACCGGTAATAGCATCT 60  
|||||

QY 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||  
Db 61 GAGGATTTGAAGTCTGTAAAAATCCATTATGACTTTATATGGGCTGCAAGAACAC 120  
|||||

QY 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||  
Db 121 TTGTCATTTAAGCATGAGGAGCTTTTCACTATATCCGACGTTTTTGGCCAACTCGACGTC 180  
|||||

QY 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
|||||  
Db 181 CAGCTGGTCAAGTCTAGAGTAGTAGAAGCGTATGAATTCACG 228  
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BASE COUNT

ORIGIN 1 bp upstream of HindIII site.

Query Match 98.6%; Score 224.8; DB 8; Length 2811;  
Best Local Similarity 99.1%; Pred. No. 6.6e-52;  
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCTGTATCTTTCAACTCTCTGAGCGCAATTAATACCGGTAAATAGCATCT 60  
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Db 631 CCCCCTGTATCTTTCAACTCTCTGAGCGCAATTAATACCGGTAAATAGCATCT 690  
|||||  
QY 61 GACGATTTGAAAGTCTGTAATAAATCCATTATGACTTTATATGGGGTGCAGAAACAC 120  
|||||  
Db 691 GACGATTTGAAAGTCTGTAATAAATCCATTATGACTTTATATGGGGTGCAGAAACAC 750  
|||||  
QY 121 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGAGCTTTTGCACATCAGCTCC 180  
|||||  
Db 751 TTTCATTTAAGCATGAGGAGCTTTTCACTATATCCGAGCTTTTGCACATCAGCTCC 810  
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QY 181 CAGCTGGTCAAAAGTCTGAGAACTAGTAGAAGCGTAAATGATCCAGC 228  
|||||  
Db 811 CAGCTGGTCAAAAGTCTGAGAACTAGTAGAAGCGTAAATGATCCAGC 858  
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RESULT 15

SCU12980  
LOCUS SCU12980 103682 bp DNA linear PLN 05-MAR-1998  
DEFINITION Saccharomyces cerevisiae chromosome I left arm sequence.  
ACCESSION U12980 U00091  
VERSION U12980.1 GI:2911250

KEYWORDS S.cerevisiae Ycr28p homolog; FLO9; GDI3; two alcohol/sorbitol dehydrogenase homologs; SIM1; CNE1; ACS1; S.pombe SPAC1P7.03 homolog; S.cerevisiae Pip2p-like transcription factor homolog; GCV3, glycine cleavage H protein; PTAL1; FUN9 transcript, essential gene; S.pombe SPAC 24B11.08c homolog; CDC24; CLN3/WHI1/DAF2; CYC3; Pyk1; S.cerevisiae ORF 06283 homolog; Xenopus laevis GTP-binding protein DRG homolog; FUN12 transcript, essential gene; FUN19 transcript, S.cerevisiae orf 06265 homolog; FUN53 transcript, essential gene; FUN20 transcript, essential gene; S.pombe SPAC 8A4.06 homolog; SNE1; MYO2; S.cerevisiae ORF 06159 homolog; DR52; MAK16; LIE1.

SOURCE Saccharomyces cerevisiae (baker's yeast)

ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (sites)

AUTHORS Nagasul.T. and Hall.B.D.

TITLE Nucleotide sequence of the GDH gene coding for the NADP-specific glutamate dehydrogenase of Saccharomyces cerevisiae

JOURNAL Gene 37 (1-3), 247-253 (1985)

MEDLINE 86031359

PUBMED 2932370

REFERENCE 2 (sites)

AUTHORS Dumont.M.E., Ernst.J.F., Hampsey.D.M. and Sherman.F.

TITLE Identification and sequence of the gene encoding cytochrome c heme lyase in the yeast Saccharomyces cerevisiae

JOURNAL EMBO J. 6 (1), 235-241 (1987)

MEDLINE 87218469

PUBMED 3034577

REFERENCE 3 (sites)

AUTHORS Miyamoto.S., Ohya.Y., Ohsumi.Y. and Anraku.Y.

TITLE Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces cerevisiae

JOURNAL Gene 54 (1), 125-132 (1987)

MEDLINE 87277425

PUBMED 3301539

REFERENCE 4 (sites)

AUTHORS Wickner.R.B.

TITLE Host function of MAK16: G1 arrest by a mak16 mutant of Saccharomyces cerevisiae

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6007-6011 (1988)

MEDLINE 88320371

PUBMED 3045810

REFERENCE 5 (sites)

AUTHORS Nash.R., Tokiwa.G., Anand.S., Erickson.K. and Fitcher.A.B.  
TITLE The WHI1+ gene of Saccharomyces cerevisiae tethers cell division to cell size and is a cyclin homolog  
JOURNAL EMBO J. 7 (13), 4335-4346 (1988)  
MEDLINE 89210821  
PUBMED 2907481  
REFERENCE 6 (sites)  
AUTHORS McNally.T., Purvis.I.J., Fothergill-Gilmore.L.A. and Brown.A.J.  
TITLE The yeast pyruvate kinase gene does not contain a string of non-preferred codons: revised nucleotide sequence  
FEBS Lett. 247 (2), 312-316 (1989)  
MEDLINE 89232143  
PUBMED 2653861  
REFERENCE 7 (sites)  
AUTHORS Harris.S.D., Cheng.J., Pugh.T.A. and Pringle.J.R.  
TITLE Molecular analysis of Saccharomyces cerevisiae chromosome I. On the number of genes and the identification of essential genes using temperature-sensitive-lethal mutations  
J. Mol. Biol. 225 (1), 53-65 (1992)  
MEDLINE 92260538  
PUBMED 1583694  
REFERENCE 8 (sites)  
AUTHORS Oliver.S.G., van der Aart.Q.J., Agostoni-Carbone.M.L., Aigle.M., Alberghina.L., Alexandraki.D., Antoine.G., Anwar.R., Ballesta.J.P., Benit.P. et al.  
TITLE The complete DNA sequence of yeast chromosome III  
JOURNAL Nature 357 (6373), 38-46 (1992)  
MEDLINE 92244356  
PUBMED 1574125  
REFERENCE 9 (sites)  
AUTHORS Gerst.J.E., Rodgers.S., Riggs.M. and Wigler.M.  
TITLE SNE1, a yeast homolog of the synaptic vesicle-associated membrane protein/synaptobrevin gene family: genetic interactions with the RAS and CAP genes  
Proc. Natl. Acad. Sci. U.S.A. 89 (10), 4338-4342 (1992)  
MEDLINE 92262435  
PUBMED 1316605  
REFERENCE 10 (sites)  
AUTHORS O'Connor.J.P. and Peebles.C.L.  
TITLE PTAL, an essential gene of Saccharomyces cerevisiae affecting pre-tRNA processing  
Mol. Cell. Biol. 12 (9), 3843-3856 (1992)  
MEDLINE 92375052  
PUBMED 1508188  
REFERENCE 11 (sites)  
AUTHORS De Virgilio.C., Burckert.N., Barth.G., Neuhaus.J.M., Boller.T. and Wiemken.A.  
TITLE Cloning and disruption of a gene required for growth on acetate but not on ethanol: the acetyl-coenzyme A synthetase gene of Saccharomyces cerevisiae  
Yeast 8 (12), 1043-1051 (1992)  
MEDLINE 93190633  
PUBMED 1363452  
REFERENCE 12 (sites)  
AUTHORS de Virgilio.C., Burckert.N., Neuhaus.J.M., Boller.T. and Wiemken.A.  
TITLE CNE1, a Saccharomyces cerevisiae homologue of the genes encoding mammalian calnexin and calreticulin  
Yeast 9 (2), 185-188 (1993)  
MEDLINE 93220396  
PUBMED 9465605  
REFERENCE 13 (sites)  
AUTHORS Teunissen.A.W., Holub.E., van der Hucht.J., van den Berg.J.A. and Steensma.H.Y.  
TITLE Sequence of the open reading frame of the FLO1 gene from Saccharomyces cerevisiae  
Yeast 9 (4), 423-427 (1993)  
MEDLINE 93289821  
PUBMED 8511970  
REFERENCE 14 (sites)  
AUTHORS Ripmaster.T.L., Vaughn.G.P. and Woolford.J.L. Jr.  
TITLE DR51 to DR57, novel genes required for ribosome assembly and function in Saccharomyces cerevisiae  
Mol. Cell. Biol. 13 (12), 7901-7912 (1993)  
JOURNAL

